GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 14, 2003, 05:40:35 ; Search time 257 Seconds
(without alignments)
2260.761 Million cell updates/sec

Title: US-09-698-781-3
Perfect score: 258
Sequence: 1 MKQILHPALETTAMTLFPVL.....KHQLVRDSCKASCNCSNSIY 258

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1201076

Minimum DB seq length: 20
Maximum DB seq length: 99

Post-processing: Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US09698781/runat_07032003_083809_6932/app_query.fasta_1.455
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=oli.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=100 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=30 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=20 -MAXLEN=99
-USER=US09698781_@CGN_1_1_263_@runat_07032003_083809_6932 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13	5.0	65	24	ABN50999	Mouse spliced tran
c	2	7	2.7	31	21	AAA05906	Group B Streptococ
	3	7	2.7	41	21	AAZ87893	AMG variant constr
c	4	7	2.7	76	19	AAV01541	LEU2 gene PCR prim
c	5	7	2.7	76	19	AAT96372	Yeast LEU2 gene pr
c	6	6	2.3	20	20	AAX38442	E. coli K12 R2 ant
	7	6	2.3	20	24	ABL43741	Human chromosome 1
c	8	6	2.3	21	20	AAX32872	TFO B14 sequence.
c	9	6	2.3	21	22	AAF97146	Human gene single
c	10	6	2.3	22	14	AAQ52863	Cytomegalovirus ta
c	11	6	2.3	23	24	ABK95528	Novel G-protein co
	12	6	2.3	24	24	ABQ00653	Oligonucleotide ad
	13	6	2.3	24	24	ABQ05246	Oligonucleotide ad
c	14	6	2.3	24	24	ABQ05287	Oligonucleotide ad
	15	6	2.3	24	24	ABQ11574	Oligonucleotide ad
c	16	6	2.3	24	24	ABQ11615	Oligonucleotide ad
c	17	6	2.3	25	19	AAV53748	Nucleotide sequenc
	18	6	2.3	25	24	ABQ64866	Human KTOM1a porti
	19	6	2.3	25	24	ABQ64867	Human KTOM1a porti
	20	6	2.3	25	24	ABQ64868	Human KTOM1a porti
	21	6	2.3	25	24	ABQ64869	Human KTOM1a porti
	22	6	2.3	25	24	ABQ64870	Human KTOM1a porti
	23	6	2.3	25	24	ABQ64871	Human KTOM1a porti
	24	6	2.3	25	24	ABQ64872	Human KTOM1a porti
	25	6	2.3	25	24	ABQ64873	Human KTOM1a porti
	26	6	2.3	25	24	ABQ13110	Oligonucleotide ad
c	27	6	2.3	25	24	ABQ13151	Oligonucleotide ad
	28	6	2.3	25	24	ABA95724	PCR primer EF-1alp
c	29	6	2.3	27	18	AAT84966	PCR primer 3F used
c	30	6	2.3	27	18	AAV00582	PCR primer 3F used
c	31	6	2.3	27	18	AAT61708	Prostatic specific
c	32	6	2.3	27	19	AAV17629	Homo sapiens argin
c	33	6	2.3	27	20	AAX77311	Arginase II cDNA c
c	34	6	2.3	27	21	AAA08065	Human arginase II
c	35	6	2.3	27	24	AAI72342	Human arginase II
c	36	6	2.3	28	17	AAT17983	pBR322 rapid site
	37	6	2.3	28	18	AAT76178	Human IL3 receptor
	38	6	2.3	28	20	AAX53975	Human IL-3 recepto
	39	6	2.3	28	21	AAF19541	Human IL3 receptor
	40	6	2.3	28	21	AAA33419	Low adenosine anti
	41	6	2.3	28	24	ABL31816	Human CYP2B6 PCR p
c	42	6	2.3	30	18	AAT43372	SAR element PCR pr
c	43	6	2.3	30	19	AAV32379	Adenovirus type 5
c	44	6	2.3	30	21	AAA87994	Scaffold attachmen
c	45	6	2.3	30	21	AAA59041	PCR primer used to
	46	6	2.3	30	22	AAH27041	Interleukin 10 rec
	47	6	2.3	30	22	AAC63904	Chromobacterium SC
	48	6	2.3	30	22	AAC63905	Chromobacterium SC
c	49	6	2.3	30	24	ABA94250	Adenovirus 5 fiber
	50	6	2.3	32	14	AAQ47880	SSP for flavonoid-
	51	6	2.3	32	21	AAZ45458	Sequence of eosino
c	52	6	2.3	32	24	ABK14781	Human protein disu
	53	6	2.3	33	24	ABQ76047	Human actin simila
	54	6	2.3	34	21	AAA29079	Antisense primer t
	55	6	2.3	34	22	AAH76744	Actin 41 PCR prime
c	56	6	2.3	35	22	AAD16202	Human uPAR gene "1
	57	6	2.3	35	22	AAH75791	Receptor 222 codin
	58	6	2.3	38	19	AAV85593	LRP5 exon primer E
	59	6	2.3	39	22	AAH02123	Candida lusitaniae
c	60	6	2.3	40	17	AAT69524	Plasmid p182SfiI c
c	61	6	2.3	40	20	AAX88949	Circular plasmid e
	62	6	2.3	40	21	AAZ95811	Polynucleotide seq
c	63	6	2.3	40	24	ABA98225	Oligonucleotide 48
	64	6	2.3	44	15	AAQ73449	PCR primer for pBR
	65	6	2.3	45	21	AAA70359	Bordeteila pertuss
c	66	6	2.3	47	21	AAZ67884	Human map-related
	67	6	2.3	47	21	AAZ68662	Human map-related

c	68	6	2.3	48	19	AAV41151	Primer CAPL-rib-1
c	69	6	2.3	48	20	AAX17705	US5877308 Seq ID 1
c	70	6	2.3	49	20	AAX80040	B. thuringiensis c
c	71	6	2.3	49	21	AAA08150	B. thuringiensis c
	72	6	2.3	50	20	AAZ34204	Human PRO865 hybri
c	73	6	2.3	50	20	AAX52172	Synthetic plasmid
	74	6	2.3	50	21	AAC78820	Human PRO541 hybri
	75	6	2.3	50	22	AAL33646	Human SNP oligonuc
c	76	6	2.3	50	22	AAI73383	Human silent SNP c
	77	6	2.3	51	21	AAA76588	Human clone cg2142
	78	6	2.3	51	21	AAA76589	Human clone cg2142
c	79	6	2.3	51	22	AAL26961	Human SNP oligonuc
	80	6	2.3	51	22	AAL27553	Human SNP oligonuc
	81	6	2.3	51	22	AAL30552	Human SNP oligonuc
	82	6	2.3	51	22	AAL30772	Human SNP oligonuc
c	83	6	2.3	51	22	AAL32547	Human SNP oligonuc
c	84	6	2.3	51	22	AAI73382	Human silent SNP c
c	85	6	2.3	51	22	AAI73814	Human silent SNP c
c	86	6	2.3	51	22	AAI73815	Human silent SNP c
c	87	6	2.3	51	22	AAI73940	Human silent SNP c
c	88	6	2.3	51	22	AAI73941	Human silent SNP c
	89	6	2.3	51	22	AAI74100	Human silent SNP c
	90	6	2.3	51	22	AAI74101	Human silent SNP c
	91	6	2.3	51	22	AAI78372	Human silent SNP c
	92	6	2.3	51	22	AAI78373	Human silent SNP c
c	93	6	2.3	51	22	AAH79416	Human DNA containi
	94	6	2.3	51	22	AAH79528	Human DNA containi
c	95	6	2.3	51	22	AAH39100	Human SNP flanking
c	96	6	2.3	51	22	AAH40348	Human SNP flanking
c	97	6	2.3	52	22	AAH50319	Bacterial 23S/5S R
	98	6	2.3	57	21	AAC52866	Arabidopsis thalia
	99	6	2.3	60	10	AAN90880	Synthetic oligonuc
	100	6	2.3	60	24	ABN36373	Human spliced tran

ALIGNMENTS

RESULT 1
ABN50999
ID ABN50999 standard; DNA; 65 BP.
XX
AC ABN50999;
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:23747.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Mus musculus.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -
XX
PS Example 1; SEQ ID 23747; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 65 BP; 26 A; 13 C; 15 G; 11 T; 0 other;

Alignment Scores:

Pred. No.:	0.000237	Length:	65
Score:	13.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.04%	Indels:	0
DB:	24	Gaps:	0

US-09-698-781-3 (1-258) x ABN50999 (1-65)

```
Qy      52 GlnArgGluIleValAsnLysHisAsnGluLeuArgArg 64
           |||||||||||||||||||||||||||||||||||||||
Db       1 CAAAGAGAGATCGTAAATAAACACAATGAGCTGAGGAGA 39
```

RESULT 2
AAA05906/c
ID AAA05906 standard; DNA; 31 BP.
XX
AC AAA05906;
XX
DT 30-MAY-2000 (first entry)
XX
DE Group B Streptococcus nucleotide sequence PCR primer #23.
XX
KW Group B Streptococcus; Streptococcus agalactiae; protein antigen;
KW vaccine; screening; immunogen; detection; diagnosis; infection;
KW antibody; affibody; antibacterial; PCR primer; ss.
XX
OS Streptococcus agalactiae.
XX
PN WO200006736-A2.
XX
PD 10-FEB-2000.
XX
PF 27-JUL-1999; 99WO-GB02444.
XX
PR 27-JUL-1998; 98GB-0016335.
PR 19-MAR-1999; 99US-0125163.
XX
PA (MICR-) MICROBIAL TECHNICS LTD.
XX
PI Le Page RWF, Wells JM, Hanniffy SB;
XX
DR WPI; 2000-195299/17.
XX

PT New Group B Streptococcus protein, useful as vaccine, for diagnosis of
PT Streptococcal infections and for screening of antibodies or affibodies
XX
PS Example 2; Page 52; 123pp; English.
XX
CC AAA05803 to AAA05872 encode proteins, polypeptides and peptides (given
CC in AAY91275 to AAY91343) isolated from Group B Streptococcus (GBS), also
CC known as Streptococcus agalactiae. The GBS polynucleotides and
CC polypeptides have antibacterial activity. Immunogenic compositions
CC comprising GBS polynucleotides or polypeptides can be used as vaccines
CC and for the treatment or prophylaxis of GBS infection. The
CC polynucleotides and polypeptides can also be used in the detection of GBS
CC and for screening DNA encoding bacterial cell envelope associated or
CC secreted antigens in gram positive bacteria. AAA05873 to AAA05941
CC represent primers used in the exemplification of the present invention.
XX
SQ Sequence 31 BP; 2 A; 9 C; 7 G; 13 T; 0 other;

Alignment Scores:

Pred. No.:	98.9	Length:	31
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.71%	Indels:	0
DB:	21	Gaps:	0

US-09-698-781-3 (1-258) x AAA05906 (1-31)

```
Qy     78 TrpAsnLysGluAlaAlaAla 84
          |||||||||||||||||||||
Db     22 TGGAACAAAGAAGCGGCCGCA 2
```

RESULT 3
AAZ87893
ID AAZ87893 standard; DNA; 41 BP.
XX
AC AAZ87893;
XX
DT 22-MAY-2000 (first entry)
XX
DE AMG variant constructing primer Hk3-K352Q.
XX
KW Glucoamylase; variant; starch conversion; saccharification; ethanol;
KW fuel; beverage; fermentation; citric acid; ascorbic acid; thermostable;
KW G2 glucoamylase; fungal; AMG; PCR primer; ss.
XX
OS Aspergillus niger.
XX
PN WO200004136-A1.
XX
PD 27-JAN-2000.
XX
PF 09-JUL-1999; 99WO-DK00392.
XX
PR 15-JUL-1998; 98DK-0000937.
PR 17-DEC-1998; 98DK-0001667.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Nielsen BR, Svendsen A, Pedersen H, Vind J, Hendriksen HV;
PI Frandsen TP;
XX
DR WPI; 2000-182412/16.
XX
PT Variant fungal glucoamylases with improved thermostability and
PT increased specific activity, useful in saccharification processes -
XX
PS Example 3; Page 60; 116pp; English.
XX
CC The invention relates to variant fungal glucoamylases. The variants
CC comprise specific mutations in the parent G2 glucoamylase (AMG) sequence
CC (AAY77740) from A. niger (see AAZ87842 for speciifc positions of the
CC mutations). The glucoamylase variants are useful in a starch conversion
CC process, especially continuous process which include a continuous
CC saccharification process. The variants can be used for producing
CC oligosaccharides, specialty syrups, or ethanol for fuel or beverages.
CC They can also be used in fermentation processes for producing organic
CC compounds such as citric acid, ascorbic acid, lysine and glutamic acid.
CC The glucoamylase variants have improved thermostability and/or increased
CC specific activity. This is advantageous in industrial saccharification
CC processes. The risk of microbial contamination is also reduced when
CC carrying the saccharification process at temperatures above 63 plusoC.
CC An increased specific activity towards short chain saccharides such as
CC maltose (without reducing the activity towards oligosaccharides) would
CC also permit using a lower enzyme dosage and/or shorter process times.
CC Sequences AAZ87844-87911 represent PCR primers used to prepare DNA
CC fragments carrying the AMG gene. This is used for the construction, by
CC PCR shuffling spiked with DNA oligos, of A. niger AMG variants having
CC improved thermostability.
XX
SQ Sequence 41 BP; 7 A; 11 C; 11 G; 12 T; 0 other;

Alignment Scores:

Pred. No.:	128	Length:	41
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.71%	Indels:	0
DB:	21	Gaps:	0

US-09-698-781-3 (1-258) x AAZ87893 (1-41)

```
Qy     24 ValAlaGlyLeuLeuProSer 30
          ||||||||||||||||||||
Db      4 GTCGCTGGACTTCTTCCAAGC 24
```

RESULT 4
AAV01541/c
ID AAV01541 standard; DNA; 76 BP.
XX
AC AAV01541;
XX
DT 08-JUN-1998 (first entry)
XX
DE LEU2 gene PCR primer KO-3'.
XX
KW Acylcoenzyme A:cholesterol acyltransferase; ACAT I;
KW ACAT related gene product 1; ARGP-1; ARP-2; sterol esterification;
KW inhibitor; atherosclerosis; hyperlipidaemia; LEU2 gene; PCR; primer;
KW ss.
XX
OS Synthetic.
XX
PN WO9745439-A1.
XX
PD 04-DEC-1997.
XX
PF 30-MAY-1997; 97WO-US09460.
XX
PR 30-MAY-1996; 96US-0657620.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Sturley SL;
XX
DR WPI; 1998-032573/03.
XX
PT DNA encoding acylcoenzyme A: cholesterol acyltransferase II or
PT III - useful to identify inhibitors for treatment of
PT atherosclerosis or hyperlipidaemia
XX
PS Disclosure; Page 68; 121pp; English.
XX
CC Primers KO-3' and KO-5' (see AAV01540) were used in a PCR with LEU2
CC gene as template to produce a selectable yeast gene flanked by
CC acyl-coenzyme A:cholesterol acyltransferase II gene sequences

CC sequences. This was used to transform a derivative of yeast strain
CC 5051, heterozygous for the areldeltaNA allele. Integrants at the
CC ARE2 locus were identified by further PCR (see AAV01542-44). The
CC invention relates to isolated nucleic acids (see AAV01533-35) coding
CC for human and mouse acylcoenzyme A:cholesterol acyltransferase II
CC and III (see AAW43406-08), also designated ACAT related gene products
CC (ARGP) 1 and 2. These can be used to identify inhibitors useful in
CC the treatment of atherosclerosis and hyperlipidaemia.
XX
SQ Sequence 76 BP; 21 A; 17 C; 18 G; 20 T; 0 other;

Alignment Scores:

Pred. No.:	228	Length:	76
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.71%	Indels:	0
DB:	19	Gaps:	0

US-09-698-781-3 (1-258) x AAV01541 (1-76)

```
Qy    248 LysAlaSerCysAsnCysSer 254
          |||||||||||||||||||||
Db     44 AAGGCATCCTGCAACTGTTCT 24
```

RESULT 5
AAT96372/c
ID AAT96372 standard; DNA; 76 BP.
XX
AC AAT96372;
XX
DT 21-MAY-1998 (first entry)
XX
DE Yeast LEU2 gene primer KO-3'.
XX
KW Acyl-coenzyme A: cholesterol acyltransferase 2; ARE2; yeast;
KW sterol; esterification; arteriosclerosis; hyperlipidaemia;
KW antifungal; fungicide; LEU2 gene; selectable marker; PCR; primer;
KW ss.
XX
OS Synthetic.
OS Saccharomyces cerevisiae.
XX
PN WO9745536-A1.
XX
PD 04-DEC-1997.
XX
PF 30-MAY-1997; 97WO-US09160.
XX
PR 30-MAY-1996; 96US-0657621.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
PA (INDV) UNIV INDIANA FOUND.
XX
PI Bard M, Sturley SL, Yang H;
XX
DR WPI; 1998-032644/03.
XX
PT Yeast acyl:coenzyme A:cholesterol acyl:transferase related enzyme I
PT and II - useful to identify inhibitor for treatment of
PT hyperlipidaemia, arteriosclerosis and fungal invasion
XX
PS Example 1; Page 27; 111pp; English.
XX
CC Primers KO-3' and KO-5 (see AAT96371) were used in a PCR with LEU2
CC gene as template to produce a selectable yeast gene flanked by
CC acyl-coenzyme A:cholesterol acyltransferase II (ARE2) gene
CC sequences (see AAT96370). This was used to transform a derivative
CC of yeast strain 5051, heterozygous for the areldeltaNA allele.
CC Integrants at the ARE2 locus were identified by further PCR (see
CC AAT96373-74 and AAV04000). The invention relates to novel yeast
CC ARE1 and ARE2 proteins (see AAW38417-18) and their use for
CC identifying inhibitors useful in the treatment of hyperlipidaemia,
CC arteriosclerosis and fungal invasion.
XX
SQ Sequence 76 BP; 21 A; 17 C; 18 G; 20 T; 0 other;

Alignment Scores:

Pred. No.:	228	Length:	76
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.71%	Indels:	0
DB:	19	Gaps:	0

US-09-698-781-3 (1-258) x AAT96372 (1-76)

```
Qy    248 LysAlaSerCysAsnCysSer 254
          |||||||||||||||||||||
Db     44 AAGGCATCCTGCAACTGTTCT 24
```

RESULT 6
AAX38442/c
ID AAX38442 standard; DNA; 20 BP.
XX
AC AAX38442;
XX
DT 16-JUN-1999 (first entry)
XX
DE E. coli K12 R2 antisense oligonucleotide 34.
XX
KW Microorganism inhibitor; antisense; nuclease resistant; treatment;
KW ribonucleotide reductase; secA gene; pathological condition; R1 subunit;
KW antimicrobial agent; crop protection; primer; R2 subunit; ss.
XX
OS Synthetic.
OS Escherichia coli.
XX
PN WO9902673-A2.
XX
PD 21-JAN-1999.
XX
PF 10-JUL-1998; 98WO-CA00666.
XX
PR 10-JUL-1997; 97US-0052160.
XX
PA (GENE-) GENESENSE TECHNOLOGIES INC.
XX
PI Dugourd D, Wright JA, Young AH;
XX
DR WPI; 1999-120874/10.
XX
PT New oligonucleotides complementary to RR or SecA genes - useful to
PT inhibit growth of microorganisms
XX
PS Disclosure; Page 22; 103pp; English.
XX
CC This invention describes novel antisense oligonucleotides
CC (AAX38301-X38552) which are nuclease resistant, and comprises about 3-50
CC nucleotides complementary to the ribonucleotide reductase gene or the
CC secA gene of a microorganism. The antisense oligonucleotides are used to
CC treat mammalian pathological conditions mediated by microorganisms. The
CC oligonucleotides are particularly useful as antimicrobial agents in crop
CC protection.
XX
SQ Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 other;

Alignment Scores:

Pred. No.:	638	Length:	20
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.33%	Indels:	0
DB:	20	Gaps:	0

US-09-698-781-3 (1-258) x AAX38442 (1-20)

```
Qy    159 SerSerTyrLeuValGly 164
          |||||||||||||||||
Db     20 AGTTCTTATCTGGTCGGG 3

RESULT 7
ABL43741
ID   ABL43741 standard; DNA; 20 BP.
XX
AC   ABL43741;
XX
DT   11-APR-2002  (first entry)
XX
DE   Human chromosome 1p36-35 PCR primer SEQ ID NO:785.
XX
KW   Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
KW   genome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001321190-A.
XX
PD   20-NOV-2001.
XX
PF   12-MAR-2001; 2001JP-0068285.
XX
PR   10-MAR-2000; 2000JP-0066716.
XX
PA   (RIKA ) RIKAGAKU KENKYUSHO.
PA   (GENO-) GENOTEX YG.
XX
DR   WPI; 2002-144136/19.
XX
PT   Arraying genome clones  -
XX
PS   Claim 4; Page 20; 528pp; Japanese.
XX
CC   The present invention describes a method of arraying genome clones. The
CC   method comprises: (a) clones of the genomic libraries contained in
CC   multiwell plates numbered for discrimination are mixed in each of the
CC   multiwell plates; (b) a primer designed based on the chromosome marker
CC   sequence is added to the mixture to carry out an amplification reaction;
CC   (c) a signal corresponding to the marker is detected from the resultant
CC   amplified product to specify the discrimination Nos. of the multiwell
CC   plates containing the clones having said marker sequence; (d) the order
CC   of the markers is changed so that the same discrimination Nos. succeed to
CC   the maximum in the specified discrimination Nos. to array the multiwell
CC   plates; (e) the clones in the multiwell plates of the specified
CC   discrimination Nos. are mixed respectively in each wells of longitudinal
CC   and lateral directions; (f) the mixed clones are cultured and the
CC   resultant cultures are amplified by using the above primer; (g) signals
CC   are detected from the amplified products; (h) the clones in the multiwell
CC   plates are specified from the detected result; and (i) the clones are
CC   reconstituted as the positions on the chromosome and arrayed. The
CC   microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC   PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC   represent PCR primers for human chromosome 21q22.1, which are
CC   specifically claimed for use in the present invention.
XX
SQ   Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 other;

Alignment Scores:
Pred. No.:              638          Length:        20
Score:                  6.00         Matches:       6
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            2.33%        Indels:        0
DB:                     24           Gaps:          0

US-09-698-781-3 (1-258) x ABL43741 (1-20)

Qy     38 AspProAlaPheThrAla 43
          ||||||||||||||||||

Db      1 GATCCTGCCTTTACTGCT 18

RESULT 8
AAX32872/c
ID   AAX32872 standard; DNA; 21 BP.
XX
AC   AAX32872;
XX
DT   28-JUN-1999  (first entry)
XX
DE   TFO B14 sequence.
XX
KW   Triplex-forming oligonucleotide; TFO; promoter region; pre-S gene;
KW   inhibition; hepatitis B virus; HBV adr subtype; DR region; ss.
XX
OS   Synthetic.
OS   Hepatitis b virus.
XX
PN   WO9920641-A1.
XX
PD   29-APR-1999.
XX
PF   19-OCT-1998;   98WO-CN00248.
XX
PR   21-OCT-1997;   97CN-0106667.
XX
PA   (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
XX
PI   Lu C;
XX
DR   WPI; 1999-288270/24.
XX
PT   Triplex-forming oligonucleotides, useful for, e.g. inhibition of
PT   hepatitis B virus (HBV)
XX
PS   Disclosure; Page 12; 39pp; Chinese.
XX
CC   The invention provides triplex-forming oligonucleotides (TFO) and their
CC   modified derivatives. TFO B1-B5 (AAX32862-866) can bind with the
CC   promoter region of pre-S gene in inhibition of hepatitis B virus (HBV)
CC   adr subtype and TFO B11, B12 and B15 (AAX32868-870) can bind with DR
CC   region of HBV. The oligonucleotides are useful for inhibition of HBV and
CC   as drug in treatment of hepatitis B. Since the length of the
CC   oligonucleotides can be suitably increased, the stability and specificity
CC   of the formed triplex DNA with 2 similar homopoly purine/homopoly
CC   pyrimidine fragments are higher. Triplex formation is specifically
CC   targeting on the HBV gene expression, DNA replication and reproduction,
CC   or to produce (DNA)2:RNA hybrid triplex with target sequence of RNA in
CC   stopping RNA reverse transcription, so there is little effect on the
CC   human cells. Such olgionucleotides are chemically modified by
CC   3'-terminal monophosphorylation, leading to more significant inhibition
CC   due to their higher stability, and the degradation products of the
CC   modified oligonucleotides are not toxic to the body.
XX
SQ   Sequence 21 BP; 5 A; 2 C; 14 G; 0 U; 0 other;

Alignment Scores:
Pred. No.:              668          Length:        21
Score:                  6.00         Matches:       6
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            2.33%        Indels:        0
DB:                     20           Gaps:          0

US-09-698-781-3 (1-258) x AAX32872 (1-21)

Qy    116 SerSerAlaProSerSer 121
          |||||||||||||||||
Db     18 TCCTCGGCCCCCTCCTCT 1

RESULT 9
AAF97146/c
ID   AAF97146 standard; DNA; 21 BP.
```

```
XX
AC   AAF97146;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #1907.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,A)
FT                   /*tag= a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US24503.
XX
PR   10-SEP-1999;   99US-0153357.
PR   26-JUL-2000; 2000US-0220947.
PR   16-AUG-2000; 2000US-0225724.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  McCarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis -
XX
PS   Examples; Page 178; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism
CC   and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification.
XX
SQ   Sequence 21 BP; 8 A; 4 C; 6 G; 3 T; 0 other;

Alignment Scores:
Pred. No.:                668             Length:         21
Score:                    6.00            Matches:        6
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              2.33%           Indels:         0
DB:                       22              Gaps:           0

US-09-698-781-3 (1-258) x AAF97146 (1-21)

Qy     115 MetSerSerAlaProSer 120
           ||||||||||||||||||
Db      18 ATGTCATCTGCTCCTTCT 1

RESULT 10
AAQ52863/c
ID   AAQ52863 standard; RNA; 22 BP.
XX
AC   AAQ52863;
XX
DT   26-MAY-1994  (first entry)
XX
DE   Cytomegalovirus target sequence 40.
XX
KW   RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; HnRNA;
KW   picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;
KW   papilloma virus; HPV; Epstein-Barr virus; EBV; TCLV;
KW   T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;
KW   influenza virus; HSV; herpes simplex virus; vector; immune response;
KW   antibody; ribozyme; viral RNA; treatment; ss.
XX
OS   Synthetic.
XX
PN   WO9323569-A.
XX
PD   25-NOV-1993.
XX
PF   29-APR-1993;   93WO-US04020.
XX
PR   11-MAY-1992;   92US-0882689.
PR   14-MAY-1992;   92US-0882712.
PR   14-MAY-1992;   92US-0882713.
PR   14-MAY-1992;   92US-0882714.
PR   14-MAY-1992;   92US-0882823.
PR   14-MAY-1992;   92US-0882824.
PR   14-MAY-1992;   92US-0882886.
PR   14-MAY-1992;   92US-0882888.
PR   14-MAY-1992;   92US-0882889.
PR   14-MAY-1992;   92US-0882921.
PR   14-MAY-1992;   92US-0883823.
PR   14-MAY-1992;   92US-0883849.
PR   14-MAY-1992;   92US-0884073.
PR   14-MAY-1992;   92US-0884074.
PR   14-MAY-1992;   92US-0884333.
PR   14-MAY-1992;   92US-0884422.
PR   14-MAY-1992;   92US-0884431.
PR   14-MAY-1992;   92US-0884436.
PR   14-MAY-1992;   92US-0884521.
PR   31-JUL-1992;   92US-0923738.
PR   26-AUG-1992;   92US-0936086.
PR   18-SEP-1992;   92US-0948359.
PR   15-OCT-1992;   92US-0963322.
PR   07-DEC-1992;   92US-0987129.
PR   07-DEC-1992;   92US-0987130.
PR   07-DEC-1992;   92US-0987133.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Draper KG,  Dudycz LW,  Holecek JJ,  Macejak DG,  Mamine JA;
PI   McSwiggen JA;
XX
DR   WPI; 1993-386599/48.
XX
PT   Enzymatic RNA molecules - used to inhibit viral replication,
PT   infection and gene expression
XX
PS   Claim 5; Fig 13; 287pp; English.
XX
CC   The sequences (AAQ52824-Q52890) are pref. Cytomegalovirus target
CC   sequences for enzymatic RNA molecules. The RNA molecules are
CC   complementary to a substrate binding region in the specified gene
CC   target. They also have enzymatic activity, in that they specifically
CC   cleave RNA in the target. The ERMs interfere with viral replication and
CC   therefore have anti-viral properties. They can be used to attenuate
CC   viruses to be used in vaccines.
XX
SQ   Sequence 22 BP; 5 A; 4 C; 10 G; 3 U; 0 other;

Alignment Scores:
```

```
Pred. No.:              697          Length:         22
Score:                  6.00         Matches:        6
Percent Similarity:     100.00%      Conservative:   0
Best Local Similarity:  100.00%      Mismatches:     0
Query Match:            2.33%        Indels:         0
DB:                     14           Gaps:           0

US-09-698-781-3 (1-258) x AAQ52863 (1-22)

Qy    116 SerSerAlaProSerSer 121
          ||||||||||||||||||
Db     18 TCCTCAGCACCATCCTCC 1

RESULT 11
ABK95528/c
ID   ABK95528 standard; DNA; 23 BP.
XX
AC   ABK95528;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Novel G-protein coupled receptor probe #15.
XX
KW   G protein coupled receptor; GPCR; olfactory receptor;
KW   cell signal processing disorder; metabolic pathway modulation;
KW   cardiomyopathy; atherosclerosis; diabetes; developmental disease;
KW   immune disease; taste disorder; scent detectability disorder; obesity;
KW   Burkitt's lymphoma; corticoneurogenic disease; infectious disease; pain;
KW   signal transduction pathway disorder; metabolic pathway disorder;
KW   retinal disease; metabolic disorder; cancer; Parkinson's disease;
KW   acute heart failure; urinary retention; osteoporosis; Crohn's disease;
KW   ulcer; allergy; neurological disorder; genetic disorder; transplantation;
KW   fertility; Pancreatitis; Hyperthyroidism; Endometriosis;
KW   forensic biology; transgenic animal; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200240539-A2.
XX
PD   23-MAY-2002.
XX
PF   16-OCT-2001; 2001WO-US32256.
XX
PR   16-OCT-2000; 2000US-240704P.
PR   26-OCT-2000; 2000US-243497P.
PR   31-OCT-2000; 2000US-244542P.
PR   03-NOV-2000; 2000US-245484P.
PR   12-DEC-2000; 2000US-255017P.
PR   17-JAN-2001; 2001US-262159P.
PR   22-JAN-2001; 2001US-263216P.
PR   22-JAN-2001; 2001US-263340P.
PR   25-JAN-2001; 2001US-264118P.
PR   12-FEB-2001; 2001US-268225P.
PR   15-FEB-2001; 2001US-289031P.
PR   27-JUL-2001; 2001US-308203P.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Kekuda R,  Spytek KA,  Casman SJ,  Zerhusen BD,  Li L,  Tchernev VT;
PI   Colman SD,  Ballinger RA,  Padigaru M,  Wolenc AR,  Shenoy SG;
PI   Edinger SR,  Gerlach V,  Gangolli EA,  Macdougall JR,  Smithson G;
PI   Peyman JA,  Stone DJ,  Gunther E,  Ellerman K,  Grosse WM;
PI   Alsobrook JP,  Lepley DM,  Burgess CE;
XX
DR   WPI; 2002-500205/53.
XX
PT   Novel G protein coupled receptor especially olfactory receptor
PT   polypeptides and nucleic acids for diagnosing and treating
PT   atherosclerosis, cardiomyopathy and diabetes -
XX
PS   Example 2; Page 224; 309pp; English.
XX
CC   The invention describes an isolated G protein coupled receptor X
CC   (GPCR1-12) polypeptide, especially an olfactory receptor. GPCRX
CC   polypeptides are useful for identifying an agent that binds to the
CC   polypeptide and for identifying a candidate substance or ligand molecules
CC   interacting with an olfactory receptor polypeptide. The polypeptide, (I)
CC   and (II) are also useful for treating diseases and disorders related to
CC   cell signal processing and metabolic pathway modulation e.g.
CC   cardiomyopathy, atherosclerosis and diabetes, and developmental diseases,
CC   immune diseases, taste and scent detectability disorders, Burkitt's
CC   lymphoma, corticoneurogenic disease, signal transduction pathway
CC   disorders, metabolic pathway disorders, retinal diseases, metabolic
CC   disorders, obesity, infectious disease, pain, cancer, Parkinson's
CC   disease, acute heart failure, urinary retention, osteoporosis, Crohn's
CC   disease, ulcers, allergies, neurological disorders, genetic disorders,
CC   transplantation, fertility, Pancreatitis, Hyperthyroidism and
CC   Endometriosis. GPCRX sequences are also useful for identifying a cell or
CC   tissue type in a biological sample, to amplify DNA sequences from very
CC   small biological samples such as tissues e.g. hair or skin or body fluids
CC   in forensic biology. Cells comprising (I) are useful for producing
CC   non-human transgenic animals for studying the function and/or activity of
CC   GPCRX protein and for identifying and/or evaluating modulators of GPCRX
CC   protein activity. This sequence represents a probe used to detect DNA
CC   encoding a novel G-protein coupled receptor produced from real time
CC   quantative (RTQ)-PCR.
XX
SQ   Sequence 23 BP; 5 A; 8 C; 7 G; 3 T; 0 other;

Alignment Scores:
Pred. No.:              727          Length:         23
Score:                  6.00         Matches:        6
Percent Similarity:     100.00%      Conservative:   0
Best Local Similarity:  100.00%      Mismatches:     0
Query Match:            2.33%        Indels:         0
DB:                     24           Gaps:           0

US-09-698-781-3 (1-258) x ABK95528 (1-23)

Qy     23 LeuValAlaGlyLeuLeu 28
          ||||||||||||||||||
Db     22 CTTGTAGCGGGCCTCCTG 5

RESULT 12
ABQ00653
ID   ABQ00653 standard; DNA; 24 BP.
XX
AC   ABQ00653;
XX
DT   11-JUN-2002  (first entry)
XX
DE   Oligonucleotide adapter/capture probe 644.
XX
KW   Oligonucleotide array; adapter sequence; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200216649-A2.
XX
PD   28-FEB-2002.
XX
PF   27-AUG-2001; 2001WO-US26519.
XX
PR   25-AUG-2000; 2000US-227948P.
PR   29-AUG-2000; 2000US-228854P.
XX
PA   (ILLU-) ILLUMINA INC.
XX
PI   Gunderson K;
XX
DR   WPI; 2002-292068/33.
XX
PT   Array comprising adapter sequences useful for immobilizing or detecting
PT   a target nucleic acid sequence, has different addresses comprising
PT   different specific capture probes -
XX
```

```
PS   Claim 1; Page 59; 261pp; English.
XX
CC   The invention relates to an oligonucleotide array (I) comprising at least
CC   25 different addresses (adapter sequences) with each comprising a
CC   different capture probe selected from a group consisting of the sequences
CC   given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC   nucleic acid sequence by attaching a adapter nucleic acid
CC   (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
CC   nucleic acid and contacting the modified target nucleic acid with (I).
CC   The steps of above method is useful for detecting a target nucleic acid,
CC   which further comprises detecting the presence of the modified target
CC   nucleic acid.
XX
SQ   Sequence 24 BP; 3 A; 9 C; 5 G; 7 T; 0 other;

Alignment Scores:
Pred. No.:              756          Length:        24
Score:                  6.00         Matches:       6
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            2.33%        Indels:        0
DB:                     24           Gaps:          0

US-09-698-781-3 (1-258) x ABQ00653 (1-24)

Qy     203 ProCysAlaSerCysPro 208
           ||||||||||||||||||
Db       5 CCGTGCGCTTCATGTCCT 22

RESULT 13
ABQ05246
ID   ABQ05246 standard; DNA; 24 BP.
XX
AC   ABQ05246;
XX
DT   11-JUN-2002  (first entry)
XX
DE   Oligonucleotide adapter/capture probe 5237.
XX
KW   Oligonucleotide array; adapter sequence; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200216649-A2.
XX
PD   28-FEB-2002.
XX
PF   27-AUG-2001; 2001WO-US26519.
XX
PR   25-AUG-2000; 2000US-227948P.
PR   29-AUG-2000; 2000US-228854P.
XX
PA   (ILLU-) ILLUMINA INC.
XX
PI   Gunderson K;
XX
DR   WPI; 2002-292068/33.
XX
PT   Array comprising adapter sequences useful for immobilizing or detecting
PT   a target nucleic acid sequence, has different addresses comprising
PT   different specific capture probes
XX
PS   Claim 1; Page 154; 261pp; English.
XX
CC   The invention relates to an oligonucleotide array (I) comprising at least
CC   25 different addresses (adapter sequences) with each comprising a
CC   different capture probe selected from a group consisting of the sequences
CC   given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC   nucleic acid sequence by attaching a adapter nucleic acid
CC   (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
CC   nucleic acid and contacting the modified target nucleic acid with (I).
CC   The steps of above method is useful for detecting a target nucleic acid,
CC   which further comprises detecting the presence of the modified target
CC   nucleic acid.
XX
SQ   Sequence 24 BP; 3 A; 9 C; 5 G; 7 T; 0 other;

Alignment Scores:
Pred. No.:              756          Length:        24
Score:                  6.00         Matches:       6
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            2.33%        Indels:        0
DB:                     24           Gaps:          0

US-09-698-781-3 (1-258) x ABQ05246 (1-24)

Qy     203 ProCysAlaSerCysPro 208
           ||||||||||||||||||
Db       5 CCGTGCGCTTCATGTCCT 22

RESULT 14
ABQ05287/c
ID   ABQ05287 standard; DNA; 24 BP.
XX
AC   ABQ05287;
XX
DT   11-JUN-2002  (first entry)
XX
DE   Oligonucleotide adapter/capture probe 5278.
XX
KW   Oligonucleotide array; adapter sequence; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200216649-A2.
XX
PD   28-FEB-2002.
XX
PF   27-AUG-2001; 2001WO-US26519.
XX
PR   25-AUG-2000; 2000US-227948P.
PR   29-AUG-2000; 2000US-228854P.
XX
PA   (ILLU-) ILLUMINA INC.
XX
PI   Gunderson K;
XX
DR   WPI; 2002-292068/33.
XX
PT   Array comprising adapter sequences useful for immobilizing or detecting
PT   a target nucleic acid sequence, has different addresses comprising
PT   different specific capture probes
XX
PS   Claim 1; Page 154; 261pp; English.
XX
CC   The invention relates to an oligonucleotide array (I) comprising at least
CC   25 different addresses (adapter sequences) with each comprising a
CC   different capture probe selected from a group consisting of the sequences
CC   given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC   nucleic acid sequence by attaching a adapter nucleic acid
CC   (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
CC   nucleic acid and contacting the modified target nucleic acid with (I).
CC   The steps of above method is useful for detecting a target nucleic acid,
CC   which further comprises detecting the presence of the modified target
CC   nucleic acid.
XX
SQ   Sequence 24 BP; 7 A; 5 C; 9 G; 3 T; 0 other;

Alignment Scores:
Pred. No.:              756          Length:        24
Score:                  6.00         Matches:       6
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            2.33%        Indels:        0
DB:                     24           Gaps:          0
```

```
US-09-698-781-3 (1-258) x ABQ05287 (1-24)

Qy    203 ProCysAlaSerCysPro 208
          ||||||||||||||||||
Db     20 CCGTGCGCTTCATGTCCT 3

RESULT 15
ABQ11574
ID   ABQ11574 standard; DNA; 24 BP.
XX
AC   ABQ11574;
XX
DT   11-JUN-2002  (first entry)
XX
DE   Oligonucleotide adapter/capture probe 11565.
XX
KW   Oligonucleotide array; adapter sequence; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200216649-A2.
XX
PD   28-FEB-2002.
XX
PF   27-AUG-2001; 2001WO-US26519.
XX
PR   25-AUG-2000; 2000US-227948P.
PR   29-AUG-2000; 2000US-228854P.
XX
PA   (ILLU-) ILLUMINA INC.
XX
PI   Gunderson K;
XX
DR   WPI; 2002-292068/33.
XX
PT   Array comprising adapter sequences useful for immobilizing or detecting
PT   a target nucleic acid sequence, has different addresses comprising
PT   different specific capture probes  -
XX
PS   Claim 1; Page 232; 261pp; English.
XX
CC   The invention relates to an oligonucleotide array (I) comprising at least
CC   25 different addresses (adapter sequences) with each comprising a
CC   different capture probe selected from a group consisting of the sequences
CC   given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC   nucleic acid sequence by attaching a adapter nucleic acid
CC   (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
CC   nucleic acid and contacting the modified target nucleic acid with (I).
CC   The steps of above method is useful for detecting a target nucleic acid,
CC   which further comprises detecting the presence of the modified target
CC   nucleic acid.
XX
SQ   Sequence 24 BP; 3 A; 9 C; 5 G; 7 T; 0 other;

Alignment Scores:
Pred. No.:              756          Length:        24
Score:                  6.00         Matches:       6
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            2.33%        Indels:        0
DB:                     24           Gaps:          0

US-09-698-781-3 (1-258) x ABQ11574 (1-24)

Qy    203 ProCysAlaSerCysPro 208
          ||||||||||||||||||
Db      5 CCGTGCGCTTCATGTCCT 22

RESULT 16
ABQ11615/c
ID   ABQ11615 standard; DNA; 24 BP.
XX
AC   ABQ11615;
XX
DT   11-JUN-2002  (first entry)
XX
DE   Oligonucleotide adapter/capture probe 11606.
XX
KW   Oligonucleotide array; adapter sequence; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200216649-A2.
XX
PD   28-FEB-2002.
XX
PF   27-AUG-2001; 2001WO-US26519.
XX
PR   25-AUG-2000; 2000US-227948P.
PR   29-AUG-2000; 2000US-228854P.
XX
PA   (ILLU-) ILLUMINA INC.
XX
PI   Gunderson K;
XX
DR   WPI; 2002-292068/33.
XX
PT   Array comprising adapter sequences useful for immobilizing or detecting
PT   a target nucleic acid sequence, has different addresses comprising
PT   different specific capture probes  -
XX
PS   Claim 1; Page 232; 261pp; English.
XX
CC   The invention relates to an oligonucleotide array (I) comprising at least
CC   25 different addresses (adapter sequences) with each comprising a
CC   different capture probe selected from a group consisting of the sequences
CC   given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC   nucleic acid sequence by attaching a adapter nucleic acid
CC   (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
CC   nucleic acid and contacting the modified target nucleic acid with (I).
CC   The steps of above method is useful for detecting a target nucleic acid,
CC   which further comprises detecting the presence of the modified target
CC   nucleic acid.
XX
SQ   Sequence 24 BP; 7 A; 5 C; 9 G; 3 T; 0 other;

Alignment Scores:
Pred. No.:              756          Length:        24
Score:                  6.00         Matches:       6
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            2.33%        Indels:        0
DB:                     24           Gaps:          0

US-09-698-781-3 (1-258) x ABQ11615 (1-24)

Qy    203 ProCysAlaSerCysPro 208
          ||||||||||||||||||
Db     20 CCGTGCGCTTCATGTCCT 3

RESULT 17
AAV53748/c
ID   AAV53748 standard; DNA; 25 BP.
XX
AC   AAV53748;
XX
DT   20-NOV-1998  (first entry)
XX
DE   Nucleotide sequence of the linkage analysis PCR primer 10.
XX
KW   PCR; primer; amplification; linkage analysis; genetic marker; ss;
KW   progressive rod-cone degeneration disease trait; canine; chromosome 9.
XX
OS   Synthetic.
OS   Canis sp.
```

XX
PN US5804388-A.
XX
PD 08-SEP-1998.
XX
PF 10-JUL-1997; 97US-0891463.
XX
PR 10-JUL-1997; 97US-0891463.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Acland G, Aguirre G, Ray K;
XX
DR WPI; 1998-505644/43.
XX
PT Detection of canine genetic markers - linked with progressive
PT rod-cone degeneration disease
XX
PS Claim 10; Column 23; 25pp; English.
XX
CC This is the nucleotide sequence of a PCR primer used for linkage
CC analysis in the method of the invention. This involves the detection
CC of genetic markers that are genetically linked and co-segregating with
CC a progressive rod-cone degeneration disease trait in canines comprises
CC analysing chromosome 9 for polymorphisms in the prcd-informative region.
CC The method is used to determine whether a dog has a mutated progressive
CC rod-cone degeneration disease gene locus in one or both alleles.
CC Polymorphism is analysed by using primers in a nucleic acid
CC amplification reaction containing chromosome 9 to obtain an amplified
CC product.
XX
SQ Sequence 25 BP; 7 A; 7 C; 5 G; 6 T; 0 other;

Alignment Scores:

Pred. No.:	785	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.33%	Indels:	0
DB:	19	Gaps:	0

US-09-698-781-3 (1-258) x AAV53748 (1-25)

```
Qy    195 TyrValProTyrGluGln 200
          ||||||||||||||||||
Db     22 TATGTGCCTTATGAGCAA 5
```

RESULT 18
ABQ64866
ID ABQ64866 standard; DNA; 25 BP.
XX
AC ABQ64866;
XX
DT 20-AUG-2002 (first entry)
XX
DE Human KTOM1a portion (ABQ63232) probe # 1579.
XX
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200224750-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US29656.
XX
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 23-MAY-2001; 2001US-0864761.
PR 28-AUG-2001; 2001US-315676P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhang J;
XX
DR WPI; 2002-479509/51.
XX
PT New human kidney tumor overexpressed membrane (KTOM1) protein and
PT nucleic acids encoding the protein, useful for treating subjects having
PT defects in KTOM1 which can manifest as cancer of the kidney, or as a
PT disorder of e.g., liver or bone -
XX
PS Example 2; Page 364; 418pp; English.
XX
CC The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to
CC scan the nt 1-1001 portion of human KTOM1a (ABQ63232).
XX
SQ Sequence 25 BP; 3 A; 9 C; 5 G; 8 T; 0 other;

Alignment Scores:

Pred. No.:	785	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.33%	Indels:	0
DB:	24	Gaps:	0

US-09-698-781-3 (1-258) x ABQ64866 (1-25)

```
Qy    202 AlaProCysAlaSerCys 207
          ||||||||||||||||||
Db      8 GCTCCCTGCGCCTCTTGT 25
```

RESULT 19
ABQ64867
ID ABQ64867 standard; DNA; 25 BP.
XX
AC ABQ64867;
XX
DT 20-AUG-2002 (first entry)
XX
DE Human KTOM1a portion (ABQ63232) probe # 1580.
XX
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200224750-A2.
XX
PD 28-MAR-2002.
XX

PF 21-SEP-2001; 2001WO-US29656.
XX
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 23-MAY-2001; 2001US-0864761.
PR 28-AUG-2001; 2001US-315676P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhang J;
XX
DR WPI; 2002-479509/51.
XX
PT New human kidney tumor overexpressed membrane (KTOM1) protein and
PT nucleic acids encoding the protein, useful for treating subjects having
PT defects in KTOM1 which can manifest as cancer of the kidney, or as a
PT disorder of e.g., liver or bone -
XX
PS Example 2; Page 364; 418pp; English.
XX
CC The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to
CC scan the nt 1-1001 portion of human KTOM1a (ABQ63232).
XX
SQ Sequence 25 BP; 3 A; 10 C; 5 G; 7 T; 0 other;

Alignment Scores:

Pred. No.:	785	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.33%	Indels:	0
DB:	24	Gaps:	0

US-09-698-781-3 (1-258) x ABQ64867 (1-25)

```
Qy    202 AlaProCysAlaSerCys 207
          |||||||||||||||||
Db      7 GCTCCCTGCGCCTCTTGT 24
```

RESULT 20
ABQ64868
ID ABQ64868 standard; DNA; 25 BP.
XX
AC ABQ64868;
XX
DT 20-AUG-2002 (first entry)
XX
DE Human KTOM1a portion (ABQ63232) probe # 1581.
XX
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX

OS Homo sapiens.
XX
PN WO200224750-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US29656.
XX
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 23-MAY-2001; 2001US-0864761.
PR 28-AUG-2001; 2001US-315676P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhang J;
XX
DR WPI; 2002-479509/51.
XX
PT New human kidney tumor overexpressed membrane (KTOM1) protein and
PT nucleic acids encoding the protein, useful for treating subjects having
PT defects in KTOM1 which can manifest as cancer of the kidney, or as a
PT disorder of e.g., liver or bone -
XX
PS Example 2; Page 365; 418pp; English.
XX
CC The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to
CC scan the nt 1-1001 portion of human KTOM1a (ABQ63232).
XX
SQ Sequence 25 BP; 4 A; 10 C; 5 G; 6 T; 0 other;

Alignment Scores:

Pred. No.:	785	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.33%	Indels:	0
DB:	24	Gaps:	0

US-09-698-781-3 (1-258) x ABQ64868 (1-25)

```
Qy    202 AlaProCysAlaSerCys 207
          |||||||||||||||||
Db      6 GCTCCCTGCGCCTCTTGT 23
```

RESULT 21
ABQ64869
ID ABQ64869 standard; DNA; 25 BP.
XX
AC ABQ64869;
XX
DT 20-AUG-2002 (first entry)
XX

DE Human KTOM1a portion (ABQ63232) probe # 1582.
XX
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200224750-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US29656.
XX
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 23-MAY-2001; 2001US-0864761.
PR 28-AUG-2001; 2001US-315676P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhang J;
XX
DR WPI; 2002-479509/51.
XX
PT New human kidney tumor overexpressed membrane (KTOM1) protein and
PT nucleic acids encoding the protein, useful for treating subjects having
PT defects in KTOM1 which can manifest as cancer of the kidney, or as a
PT disorder of e.g., liver or bone -
XX
PS Example 2; Page 365; 418pp; English.
XX
CC The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to
CC scan the nt 1-1001 portion of human KTOM1a (ABQ63232).
XX
SQ Sequence 25 BP; 3 A; 10 C; 6 G; 6 T; 0 other;

Alignment Scores:

Pred. No.:	785	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.33%	Indels:	0
DB:	24	Gaps:	0

US-09-698-781-3 (1-258) x ABQ64869 (1-25)

```
Qy    202 AlaProCysAlaSerCys 207
          |||||||||||||||||||
Db      5 GCTCCCTGCGCCTCTTGT 22
```

RESULT 22
ABQ64870

ID ABQ64870 standard; DNA; 25 BP.
XX
AC ABQ64870;
XX
DT 20-AUG-2002 (first entry)
XX
DE Human KTOM1a portion (ABQ63232) probe # 1583.
XX
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200224750-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US29656.
XX
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 23-MAY-2001; 2001US-0864761.
PR 28-AUG-2001; 2001US-315676P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhang J;
XX
DR WPI; 2002-479509/51.
XX
PT New human kidney tumor overexpressed membrane (KTOM1) protein and
PT nucleic acids encoding the protein, useful for treating subjects having
PT defects in KTOM1 which can manifest as cancer of the kidney, or as a
PT disorder of e.g., liver or bone -
XX
PS Example 2; Page 365; 418pp; English.
XX
CC The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to
CC scan the nt 1-1001 portion of human KTOM1a (ABQ63232).
XX
SQ Sequence 25 BP; 3 A; 11 C; 5 G; 6 T; 0 other;

Alignment Scores:

Pred. No.:	785	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.33%	Indels:	0
DB:	24	Gaps:	0

US-09-698-781-3 (1-258) x ABQ64870 (1-25)

```
Qy     202 AlaProCysAlaSerCys 207
           ||||||||||||||||||
Db       4 GCTCCCTGCGCCTCTTGT 21

RESULT 23
ABQ64871
ID   ABQ64871 standard; DNA; 25 BP.
XX
AC   ABQ64871;
XX
DT   20-AUG-2002  (first entry)
XX
DE   Human KTOM1a portion (ABQ63232) probe # 1584.
XX
KW   Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW   gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW   kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200224750-A2.
XX
PD   28-MAR-2002.
XX
PF   21-SEP-2001; 2001WO-US29656.
XX
PR   21-SEP-2000; 2000US-234687P.
PR   27-SEP-2000; 2000US-236359P.
PR   04-OCT-2000; 2000GB-0024263.
PR   30-JAN-2001; 2001WO-US00661.
PR   30-JAN-2001; 2001WO-US00662.
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00666.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   30-JAN-2001; 2001WO-US00670.
PR   23-MAY-2001; 2001US-0864761.
PR   28-AUG-2001; 2001US-315676P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhang J;
XX
DR   WPI; 2002-479509/51.
XX
PT   New human kidney tumor overexpressed membrane (KTOM1) protein and
PT   nucleic acids encoding the protein, useful for treating subjects having
PT   defects in KTOM1 which can manifest as cancer of the kidney, or as a
PT   disorder of e.g., liver or bone
XX
PS   Example 2; Page 365; 418pp; English.
XX
CC   The invention relates to a novel isolated nucleic acid encoding human
CC   KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC   invention has cytostatic activity. The nucleotide may have a use in gene
CC   therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC   monitor a disease caused by altered expression of human KTOM1.
CC   Compositions comprising the nucleic acids, proteins or antibodies may be
CC   used to treat subjects having defects in KTOM1 which can manifest as
CC   cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC   heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC   function. The sequence represents a probe used in the invention to
CC   scan the nt 1-1001 portion of human KTOM1a (ABQ63232).
XX
SQ   Sequence 25 BP; 2 A; 11 C; 5 G; 7 T; 0 other;

Alignment Scores:
Pred. No.:              785          Length:        25
Score:                  6.00         Matches:       6
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            2.33%        Indels:        0
DB:                     24           Gaps:          0

US-09-698-781-3 (1-258) x ABQ64871 (1-25)

Qy     202 AlaProCysAlaSerCys 207
           ||||||||||||||||||
Db       3 GCTCCCTGCGCCTCTTGT 20

RESULT 24
ABQ64872
ID   ABQ64872 standard; DNA; 25 BP.
XX
AC   ABQ64872;
XX
DT   20-AUG-2002  (first entry)
XX
DE   Human KTOM1a portion (ABQ63232) probe # 1585.
XX
KW   Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW   gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW   kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200224750-A2.
XX
PD   28-MAR-2002.
XX
PF   21-SEP-2001; 2001WO-US29656.
XX
PR   21-SEP-2000; 2000US-234687P.
PR   27-SEP-2000; 2000US-236359P.
PR   04-OCT-2000; 2000GB-0024263.
PR   30-JAN-2001; 2001WO-US00661.
PR   30-JAN-2001; 2001WO-US00662.
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00666.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   30-JAN-2001; 2001WO-US00670.
PR   23-MAY-2001; 2001US-0864761.
PR   28-AUG-2001; 2001US-315676P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhang J;
XX
DR   WPI; 2002-479509/51.
XX
PT   New human kidney tumor overexpressed membrane (KTOM1) protein and
PT   nucleic acids encoding the protein, useful for treating subjects having
PT   defects in KTOM1 which can manifest as cancer of the kidney, or as a
PT   disorder of e.g., liver or bone
XX
PS   Example 2; Page 365; 418pp; English.
XX
CC   The invention relates to a novel isolated nucleic acid encoding human
CC   KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC   invention has cytostatic activity. The nucleotide may have a use in gene
CC   therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC   monitor a disease caused by altered expression of human KTOM1.
CC   Compositions comprising the nucleic acids, proteins or antibodies may be
CC   used to treat subjects having defects in KTOM1 which can manifest as
CC   cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC   heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC   function. The sequence represents a probe used in the invention to
CC   scan the nt 1-1001 portion of human KTOM1a (ABQ63232).
XX
```

SQ Sequence 25 BP; 2 A; 11 C; 5 G; 7 T; 0 other;

Alignment Scores:

Pred. No.:	785	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.33%	Indels:	0
DB:	24	Gaps:	0

US-09-698-781-3 (1-258) x ABQ64872 (1-25)

```
Qy    202 AlaProCysAlaSerCys 207
          |||||||||||||||||
Db      2 GCTCCCTGCGCCTCTTGT 19
```

RESULT 25
ABQ64873
ID ABQ64873 standard; DNA; 25 BP.
XX
AC ABQ64873;
XX
DT 20-AUG-2002 (first entry)
XX
DE Human KTOM1a portion (ABQ63232) probe # 1586.
XX
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200224750-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US29656.
XX
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 23-MAY-2001; 2001US-0864761.
PR 28-AUG-2001; 2001US-315676P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhang J;
XX
DR WPI; 2002-479509/51.
XX
PT New human kidney tumor overexpressed membrane (KTOM1) protein and
PT nucleic acids encoding the protein, useful for treating subjects having
PT defects in KTOM1 which can manifest as cancer of the kidney, or as a
PT disorder of e.g., liver or bone -
XX
PS Example 2; Page 365; 418pp; English.
XX
CC The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to
CC scan the nt 1-1001 portion of human KTOM1a (ABQ63232).
XX
SQ Sequence 25 BP; 1 A; 11 C; 5 G; 8 T; 0 other;

Alignment Scores:

Pred. No.:	785	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.33%	Indels:	0
DB:	24	Gaps:	0

US-09-698-781-3 (1-258) x ABQ64873 (1-25)

```
Qy    202 AlaProCysAlaSerCys 207
          |||||||||||||||||
Db      1 GCTCCCTGCGCCTCTTGT 18
```

RESULT 26
ABQ13110
ID ABQ13110 standard; DNA; 25 BP.
XX
AC ABQ13110;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 13101.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US26519.
XX
PR 25-AUG-2000; 2000US-227948P.
PR 29-AUG-2000; 2000US-228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting
PT a target nucleic acid sequence, has different addresses comprising
PT different specific capture probes -
XX
PS Claim 1; Page 251; 261pp; English.
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid
CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
CC nucleic acid and contacting the modified target nucleic acid with (I).
CC The steps of above method is useful for detecting a target nucleic acid,
CC which further comprises detecting the presence of the modified target
CC nucleic acid.
XX
SQ Sequence 25 BP; 3 A; 9 C; 5 G; 8 T; 0 other;

Alignment Scores:

Pred. No.:	785	Length:	25
Score:	6.00	Matches:	6

```
Percent Similarity:     100.00%         Conservative:  0
Best Local Similarity:  100.00%         Mismatches:    0
Query Match:            2.33%           Indels:        0
DB:                     24              Gaps:          0

US-09-698-781-3 (1-258) x ABQ13110 (1-25)

Qy    203 ProCysAlaSerCysPro 208
          ||||||||||||||||||
Db      6 CCGTGCGCTTCATGTCCT 23

RESULT 27
ABQ13151/c
ID   ABQ13151 standard; DNA; 25 BP.
XX
AC   ABQ13151;
XX
DT   11-JUN-2002  (first entry)
XX
DE   Oligonucleotide adapter/capture probe 13142.
XX
KW   Oligonucleotide array; adapter sequence; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200216649-A2.
XX
PD   28-FEB-2002.
XX
PF   27-AUG-2001; 2001WO-US26519.
XX
PR   25-AUG-2000; 2000US-227948P.
PR   29-AUG-2000; 2000US-228854P.
XX
PA   (ILLU-) ILLUMINA INC.
XX
PI   Gunderson K;
XX
DR   WPI; 2002-292068/33.
XX
PT   Array comprising adapter sequences useful for immobilizing or detecting
PT   a target nucleic acid sequence, has different addresses comprising
PT   different specific capture probes  -
XX
PS   Claim 1; Page 251; 261pp; English.
XX
CC   The invention relates to an oligonucleotide array (I) comprising at least
CC   25 different addresses (adapter sequences) with each comprising a
CC   different capture probe selected from a group consisting of the sequences
CC   given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC   nucleic acid sequence by attaching a adapter nucleic acid
CC   (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
CC   nucleic acid and contacting the modified target nucleic acid with (I).
CC   The steps of above method is useful for detecting a target nucleic acid,
CC   which further comprises detecting the presence of the modified target
CC   nucleic acid.
XX
SQ   Sequence 25 BP; 7 A; 5 C; 9 G; 4 T; 0 other;

Alignment Scores:
Pred. No.:              785             Length:        25
Score:                  6.00            Matches:       6
Percent Similarity:     100.00%         Conservative:  0
Best Local Similarity:  100.00%         Mismatches:    0
Query Match:            2.33%           Indels:        0
DB:                     24              Gaps:          0

US-09-698-781-3 (1-258) x ABQ13151 (1-25)

Qy    203 ProCysAlaSerCysPro 208
          ||||||||||||||||||
Db     21 CCGTGCGCTTCATGTCCT 4

RESULT 28
ABA95724
ID   ABA95724 standard; DNA; 25 BP.
XX
AC   ABA95724;
XX
DT   03-APR-2002  (first entry)
XX
DE   PCR primer EF-1alpha-R.
XX
KW   PCR primer; antiinflammatory; transplant; gene therapy; pancreas;
KW   organ engineering; insulin deficiency; diabetes; ss.
XX
OS   Unidentified.
XX
PN   WO200192480-A1.
XX
PD   06-DEC-2001.
XX
PF   30-MAR-2001; 2001WO-JP02765.
XX
PR   31-MAY-2000; 2000JP-0161795.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Asashima M,  Moriya N;
XX
DR   WPI; 2002-114337/15.
XX
PT   Forming vertebrate pancreas in vitro, useful in development or organ
PT   engineering, studying differentiation or formation mechanism of
PT   pancreas, transplantation, and diagnosis and treatment of pancreatic
PT   diseases  -
XX
PS   Example 4; Page 19; 37pp; Japanese.
XX
CC   The present invention relates to a method for forming a vertebrate
CC   pancreas in vitro. The method is useful in development or organ
CC   engineering, studying pancreas formation or differentiation,
CC   transplantation, and diagnosis and treatment of pancreatic diseases
CC   including gene diagnosis and gene therapy of insulin deficiency and
CC   diabetes in higher animals. The present sequence is a PCR primer, which
CC   was used in an example from the present invention.
XX
SQ   Sequence 25 BP; 2 A; 10 C; 3 G; 10 T; 0 other;

Alignment Scores:
Pred. No.:              785             Length:        25
Score:                  6.00            Matches:       6
Percent Similarity:     100.00%         Conservative:  0
Best Local Similarity:  100.00%         Mismatches:    0
Query Match:            2.33%           Indels:        0
DB:                     24              Gaps:          0

US-09-698-781-3 (1-258) x ABA95724 (1-25)

Qy     27 LeuLeuProSerPhePro 32
          |||||||||||||||||
Db      4 CTGCTGCCTTCTTTTCCA 21

RESULT 29
AAT84966/c
ID   AAT84966 standard; DNA; 27 BP.
XX
AC   AAT84966;
XX
DT   01-APR-1998  (first entry)
XX
DE   PCR primer 3F used to amplify arginase II from a cDNA library.
XX
KW   Arginase II; proline production; glutamate production; hyperarginaemia;
KW   nitric oxide biosynthesis; arginase activity; urea cycle disease;
KW   hypertension; hypotension; hyperammonaemia; prostate disease;
```

KW PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9733985-A1.
XX
PD 18-SEP-1997.
XX
PF 14-MAR-1996; 96WO-US03561.
XX
PR 14-MAR-1996; 96WO-US03561.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Dillon PJ, Vockley JG;
XX
DR WPI; 1997-470867/43.
XX
PT Polynucleotide encoding human arginase II - useful to treat,
PT diagnose and monitor, e.g. urea cycle disorders, prostatic disease,
PT hypotension and nitric oxide mediated immune and nervous diseases
XX
PS Example 1; Fig 3; 85pp; English.
XX
CC PCR primers AAT84962-74 were used to amplify human arginase II from a
CC Jurkat cell line cDNA library. The cDNA sequence of Arginase I was used
CC as a probe sequence for a computer search of cDNA databases. Several
CC expressed sequence tags with 50-60% sequence homology were identified.
CC These were combined to give a 1075 bp sequence. The above PCR primers
CC were designed to the extreme 3' and 5' ends of the consensus sequence,
CC and used to isolate arginase II. In addition to a hypothetical role in
CC the production of proline and glutamate, it is postulated that
CC arginase II may play an important role in nitric oxide biosynthesis
CC through the production of ornithine as a precursor of glutamate.
CC Arginase II, or its agonists, antagonists and fragments, are used to
CC treat conditions associated with lack of arginase activity. Compounds
CC that inhibit activation of the protein are used to treat conditions
CC associated with excess arginase activity. Typical conditions that can be
CC treated are diseases of the urea cycle, hypertension, hypotension
CC (caused by sepsis or cytokines), episodic hyperammonaemia, defective
CC synthesis of proline, glutamate, nitric oxide or ornithine,
CC hyperarginaemia and related spasticity, prostate disease (e.g. cancer,
CC prostatitis and benign hypertrophy), prostate or kidney damage, also
CC nitric oxide associated immune and nervous system diseases. The arginase
CC II cDNA is used to produce recombinant protein and for chromosome
CC identification, while its fragments are used (as primers and probes) to
CC detect arginase II-encoding sequences and to diagnose the above
CC diseases.
XX
SQ Sequence 27 BP; 6 A; 3 C; 11 G; 7 T; 0 other;

Alignment Scores:

Pred. No.:	843	Length:	27
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.33%	Indels:	0
DB:	18	Gaps:	0

US-09-698-781-3 (1-258) x AAT84966 (1-27)

```
Qy      42 ThrAlaLeuLeuThrThr 47
           ||||||||||||||||||
Db      20 ACAGCTCTGCTAACCACC 3
```

RESULT 30
AAV00582/c
ID AAV00582 standard; cDNA; 27 BP.
XX
AC AAV00582;
XX
DT 25-MAR-1998 (first entry)
XX
DE PCR primer 3F used to amplify arginase II from a cDNA library.
XX
KW Arginase II; proline production; glutamate production; hyperarginaemia;
KW nitric oxide biosynthesis; arginase activity; urea cycle disease;
KW hypertension; hypotension; hyperammonaemia; prostate disease;
KW PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9733986-A1.
XX
PD 18-SEP-1997.
XX
PF 20-AUG-1996; 96WO-US13455.
XX
PR 14-MAR-1996; 96WO-US03561.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Dillon PJ, Vockley JG;
XX
DR WPI; 1997-470868/43.
XX
PT Nucleic acid encoding human arginase II - useful for treating,
PT diagnosing and monitoring e.g. urea cycle disorders, hypotension,
PT nitric oxide-mediated immune and nervous diseases, etc
XX
PS Example 1; Fig 3; 93pp; English.
XX
CC PCR primers AAV00578-90 were used to amplify human arginase II from a
CC Jurkat cell line cDNA library. The cDNA sequence of Arginase I was used
CC as a probe sequence for a computer search of cDNA databases. Several
CC expressed sequence tags with 50-60% sequence homology were identified.
CC These were combined to give a 1075 bp sequence. The above PCR primers
CC were designed to the extreme 3' and 5' ends of the consensus sequence,
CC and used to isolate arginase II. In addition to a hypothetical role in
CC the production of proline and glutamate, it is postulated that
CC arginase II may play an important role in nitric oxide biosynthesis
CC through the production of ornithine as a precursor of glutamate.
CC Arginase II, or its agonists, antagonists and fragments, are used to
CC treat conditions associated with lack of arginase activity. Compounds
CC that inhibit activation of the protein are used to treat conditions
CC associated with excess arginase activity. Typical conditions that can be
CC treated are diseases of the urea cycle, hypertension, hypotension
CC (caused by sepsis or cytokines), episodic hyperammonaemia, defective
CC synthesis of proline, glutamate, nitric oxide or ornithine,
CC hyperarginaemia and related spasticity, prostate disease (e.g. cancer,
CC prostatitis and benign hypertrophy), prostate or kidney damage, also
CC nitric oxide associated immune and nervous system diseases. The arginase
CC II cDNA is used to produce recombinant protein and for chromosome
CC identification, while its fragments are used (as primers and probes) to
CC detect arginase II-encoding sequences and to diagnose the above
CC diseases.
XX
SQ Sequence 27 BP; 6 A; 3 C; 11 G; 7 T; 0 other;

Alignment Scores:

Pred. No.:	843	Length:	27
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.33%	Indels:	0
DB:	18	Gaps:	0

US-09-698-781-3 (1-258) x AAV00582 (1-27)

```
Qy      42 ThrAlaLeuLeuThrThr 47
           ||||||||||||||||||
Db      20 ACAGCTCTGCTAACCACC 3
```

Search completed: March 14, 2003, 05:49:58
Job time : 260 secs